

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/642,248A
Source: 1FW16
Date Processed by STIC: 9/8/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/08/2006

PATENT APPLICATION: US/10/642,248A

TIME: 11:35:33

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Output Set: N:\CRF4\09082006\J642248A.raw

3 <110> APPLICANT: DeAngelis, Paul
 4 Jing, Wei
 6 <120> TITLE OF INVENTION: TARGETED GLYCOSAMINOGLYCAN POLYMERS BY POLYMER GRAFTING AND
 METHODS OF
 7 MAKING AND USING SAME
 9 <130> FILE REFERENCE: 3554.097
 11 <140> CURRENT APPLICATION NUMBER: 10/642,248A
 12 <141> CURRENT FILING DATE: 2003-08-15
 14 <150> PRIOR APPLICATION NUMBER: 60/404,356
 15 <151> PRIOR FILING DATE: 2002-08-16
 17 <150> PRIOR APPLICATION NUMBER: 60/479,432
 18 <151> PRIOR FILING DATE: 2003-06-18
 20 <150> PRIOR APPLICATION NUMBER: 60/491,362
 21 <151> PRIOR FILING DATE: 2003-07-31
 23 <150> PRIOR APPLICATION NUMBER: 10/195,908
 24 <151> PRIOR FILING DATE: 2002-07-15
 26 <150> PRIOR APPLICATION NUMBER: 09/437,277
 27 <151> PRIOR FILING DATE: 1999-11-01
 29 <150> PRIOR APPLICATION NUMBER: 60/107,929
 30 <151> PRIOR FILING DATE: 1998-11-11
 32 <150> PRIOR APPLICATION NUMBER: 09/283,402
 33 <151> PRIOR FILING DATE: 1999-04-01
 35 <150> PRIOR APPLICATION NUMBER: 60/080,414
 36 <151> PRIOR FILING DATE: 1998-04-02
 38 <150> PRIOR APPLICATION NUMBER: 09/842,484
 39 <151> PRIOR FILING DATE: 2001-04-25
 41 <150> PRIOR APPLICATION NUMBER: 60/199,538
 42 <151> PRIOR FILING DATE: 2000-04-25
 44 <150> PRIOR APPLICATION NUMBER: 10/142,143
 45 <151> PRIOR FILING DATE: 2002-05-08
 47 <150> PRIOR APPLICATION NUMBER: 60/289,554
 48 <151> PRIOR FILING DATE: 2001-05-08
 50 <160> NUMBER OF SEQ ID NOS: 71
 52 <170> SOFTWARE: PatentIn version 3.1
 54 <210> SEQ ID NO: 1
 55 <211> LENGTH: 2920
 56 <212> TYPE: DNA
 57 <213> ORGANISM: Pasteurella multocida
 59 <400> SEQUENCE: 1
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 64 aaatgcaaaag aaaactctc agcacatctt tctgttaatt cagcacatct tctgttaaatt 180
 66 aaagaagaaa aagtcagtgt ttgcgatagt ccgttagata ttgcaacaca actgttactt 240
 68 tccaacgtaa aaaaattagt actttctgac tcggaaaaaa acacgttaaa aaataaatgg 300

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72 aaagattttc ccaaagatct ggtttttagcg cctttacctg atcatgttaa tgattttaca 420
74 tggtagacaaa agcgaaagaa aagacttggc ataaaacctg aacatcaaca tgttgggtctt 480
76 tctattatcg ttacaacatt caatcgacca gcaattttat cgattacatt agcctgttta 540
78 gtaaaccaaa aaacacatta cccgtttgaa gttatcgtga cagatgatgg tagtcaggaa 600
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82 aaagataacg gttttcaagc cagtgcgcgt cggaatatgg gattacgctt agcaaaatat 720
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124 gataacacat caattaagaa acttggcatt caaaagaaaa accattttgt ttagagtcaat 1980
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160 <211> LENGTH: 972
161 <212> TYPE: PRT
162 <213> ORGANISM: Pasteurella multocida
164 <400> SEQUENCE: 2

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Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\09082006\J642248A.raw

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167 1 5 10 15
170 Gln Leu Ala Leu Lys Leu Phe Glu Lys Ser Ala Glu Ile Tyr Gly Arg
171 20 25 30
174 Lys Ile Val Glu Phe Gln Ile Thr Lys Cys Lys Glu Lys Leu Ser Ala
175 35 40 45
178 His Pro Ser Val Asn Ser Ala His Leu Ser Val Asn Lys Glu Glu Lys
179 50 55 60
182 Val Asn Val Cys Asp Ser Pro Leu Asp Ile Ala Thr Gln Leu Leu Leu
183 65 70 75 80
186 Ser Asn Val Lys Lys Leu Val Leu Ser Asp Ser Glu Lys Asn Thr Leu
187 85 90 95
190 Lys Asn Lys Trp Lys Leu Leu Thr Glu Lys Lys Ser Glu Asn Ala Glu
191 100 105 110
194 Val Arg Ala Val Ala Leu Val Pro Lys Asp Phe Pro Lys Asp Leu Val
195 115 120 125
198 Leu Ala Pro Leu Pro Asp His Val Asn Asp Phe Thr Trp Tyr Lys Lys
199 130 135 140
202 Arg Lys Lys Arg Leu Gly Ile Lys Pro Glu His Gln His Val Gly Leu
203 145 150 155 160
206 Ser Ile Ile Val Thr Thr Phe Asn Arg Pro Ala Ile Leu Ser Ile Thr
207 165 170 175
210 Leu Ala Cys Leu Val Asn Gln Lys Thr His Tyr Pro Phe Glu Val Ile
211 180 185 190
214 Val Thr Asp Asp Gly Ser Gln Glu Asp Leu Ser Pro Ile Ile Arg Gln
215 195 200 205
218 Tyr Glu Asn Lys Leu Asp Ile Arg Tyr Val Arg Gln Lys Asp Asn Gly
219 210 215 220
222 Phe Gln Ala Ser Ala Ala Arg Asn Met Gly Leu Arg Leu Ala Lys Tyr
223 225 230 235 240
226 Asp Phe Ile Gly Leu Leu Asp Cys Asp Met Ala Pro Asn Pro Leu Trp
227 245 250 255
230 Val His Ser Tyr Val Ala Glu Leu Leu Glu Asp Asp Asp Leu Thr Ile
231 260 265 270
234 Ile Gly Pro Arg Lys Tyr Ile Asp Thr Gln His Ile Asp Pro Lys Asp
235 275 280 285
238 Phe Leu Asn Asn Ala Ser Leu Leu Glu Ser Leu Pro Glu Val Lys Thr
239 290 295 300
242 Asn Asn Ser Val Ala Ala Lys Gly Glu Gly Thr Val Ser Leu Asp Trp
243 305 310 315 320
246 Arg Leu Glu Gln Phe Glu Lys Thr Glu Asn Leu Arg Leu Ser Asp Ser
247 325 330 335
250 Pro Phe Arg Phe Phe Ala Ala Gly Asn Val Ala Phe Ala Lys Lys Trp
251 340 345 350
254 Leu Asn Lys Ser Gly Phe Phe Asp Glu Glu Phe Asn His Trp Gly Gly
255 355 360 365
258 Glu Asp Val Glu Phe Gly Tyr Arg Leu Phe Arg Tyr Gly Ser Phe Phe
259 370 375 380
262 Lys Thr Ile Asp Gly Ile Met Ala Tyr His Gln Glu Pro Pro Gly Lys

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266 Glu Asn Glu Thr Asp Arg Glu Ala Gly Lys Asn Ile Thr Leu Asp Ile
267          405          410          415
270 Met Arg Glu Lys Val Pro Tyr Ile Tyr Arg Lys Leu Leu Pro Ile Glu
271          420          425          430
274 Asp Ser His Ile Asn Arg Val Pro Leu Val Ser Ile Tyr Ile Pro Ala
275          435          440          445
278 Tyr Asn Cys Ala Asn Tyr Ile Gln Arg Cys Val Asp Ser Ala Leu Asn
279          450          455          460
282 Gln Thr Val Val Asp Leu Glu Val Cys Ile Cys Asn Asp Gly Ser Thr
283 465          470          475          480
286 Asp Asn Thr Leu Glu Val Ile Asn Lys Leu Tyr Gly Asn Asn Pro Arg
287          485          490          495
290 Val Arg Ile Met Ser Lys Pro Asn Gly Gly Ile Ala Ser Ala Ser Asn
291          500          505          510
294 Ala Ala Val Ser Phe Ala Lys Gly Tyr Tyr Ile Gly Gln Leu Asp Ser
295          515          520          525
298 Asp Asp Tyr Leu Glu Pro Asp Ala Val Glu Leu Cys Leu Lys Glu Phe
299          530          535          540
302 Leu Lys Asp Lys Thr Leu Ala Cys Val Tyr Thr Thr Asn Arg Asn Val
303 545          550          555          560
306 Asn Pro Asp Gly Ser Leu Ile Ala Asn Gly Tyr Asn Trp Pro Glu Phe
307          565          570          575
310 Ser Arg Glu Lys Leu Thr Thr Ala Met Ile Ala His His Phe Arg Met
311          580          585          590
314 Phe Thr Ile Arg Ala Trp His Leu Thr Asp Gly Phe Asn Glu Lys Ile
315          595          600          605
318 Glu Asn Ala Val Asp Tyr Asp Met Phe Leu Lys Leu Ser Glu Val Gly
319          610          615          620
322 Lys Phe Lys His Leu Asn Lys Ile Cys Tyr Asn Arg Val Leu His Gly
323 625          630          635          640
326 Asp Asn Thr Ser Ile Lys Lys Leu Gly Ile Gln Lys Lys Asn His Phe
327          645          650          655
330 Val Val Val Asn Gln Ser Leu Asn Arg Gln Gly Ile Thr Tyr Tyr Asn
331          660          665          670
334 Tyr Asp Glu Phe Asp Asp Leu Asp Glu Ser Arg Lys Tyr Ile Phe Asn
335          675          680          685
338 Lys Thr Ala Glu Tyr Gln Glu Glu Ile Asp Ile Leu Lys Asp Ile Lys
339          690          695          700
342 Ile Ile Gln Asn Lys Asp Ala Lys Ile Ala Val Ser Ile Phe Tyr Pro
343 705          710          715          720
346 Asn Thr Leu Asn Gly Leu Val Lys Lys Leu Asn Asn Ile Ile Glu Tyr
347          725          730          735
350 Asn Lys Asn Ile Phe Val Ile Val Leu His Val Asp Lys Asn His Leu
351          740          745          750
354 Thr Pro Asp Ile Lys Lys Glu Ile Leu Ala Phe Tyr His Lys His Gln
355          755          760          765
358 Val Asn Ile Leu Leu Asn Asn Asp Ile Ser Tyr Tyr Thr Ser Asn Arg
359          770          775          780

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362 Leu Ile Lys Thr Glu Ala His Leu Ser Asn Ile Asn Lys Leu Ser Gln
363 785                      790                      795                      800
366 Leu Asn Leu Asn Cys Glu Tyr Ile Ile Phe Asp Asn His Asp Ser Leu
367                      805                      810                      815
370 Phe Val Lys Asn Asp Ser Tyr Ala Tyr Met Lys Lys Tyr Asp Val Gly
371                      820                      825                      830
374 Met Asn Phe Ser Ala Leu Thr His Asp Trp Ile Glu Lys Ile Asn Ala
375                      835                      840                      845
378 His Pro Pro Phe Lys Lys Leu Ile Lys Thr Tyr Phe Asn Asp Asn Asp
379                      850                      855                      860
382 Leu Lys Ser Met Asn Val Lys Gly Ala Ser Gln Gly Met Phe Met Thr
383 865                      870                      875                      880
386 Tyr Ala Leu Ala His Glu Leu Leu Thr Ile Ile Lys Glu Val Ile Thr
387                      885                      890                      895
390 Ser Cys Gln Ser Ile Asp Ser Val Pro Glu Tyr Asn Thr Glu Asp Ile
391                      900                      905                      910
394 Trp Phe Gln Phe Ala Leu Leu Ile Leu Glu Lys Lys Thr Gly His Val
395                      915                      920                      925
398 Phe Asn Lys Thr Ser Thr Leu Thr Tyr Met Pro Trp Glu Arg Lys Leu
399                      930                      935                      940
402 Gln Trp Thr Asn Glu Gln Ile Glu Ser Ala Lys Arg Gly Glu Asn Ile
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422 aaatgtaaag aaaaactctc gaccaattct tatgtaagtg aagataaaaa aaacagtgtt      240
424 tgcgatagct cattagatat cgcaacacag ctcttacttt ccaacgtaaa aaaattaact      300
426 ctatccgaat cagaaaaaaa cagtttaaaa aataaatgga aatctatcac tgggaaaaaa      360
428 tcggagaacg cagaaatcag aaaggtggaa ctagtaccce aagattttcc taaagatctt      420
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432 agcttaggta taaagcctgt aaataagaat atcgggtcttt ctattattat tcctacattt      540
434 aatcgtagcc gtattttaga tataacgtta gcctgtttgg tcaatcagaa aacaaactac      600
436 ccatttgaag tcgttggtgc agatgatggg agtaaggaaa acttacttac cattgtgcaa      660
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440 tgtgcagtcg gaaacttagg tttacgtaca gcaaagtatg attttgtctc gattctagac      780
442 tgcgatatgg caccacaaca attatgggtt cattcttacc ttacagaact attagaagac      840
444 aatgatattg ttttaattgg acctagaaaa tatgtggata ctcataatat taccgcagaa      900
446 caattcctta acgatccata tttaatagaa tctactacct aaaccgctac aaataacaat      960
448 ccttcgatta catcaaaagg aaatatatcg ttggattgga gattagaaca tttcaaaaaa     1020
450 accgataatc tacgtctatg tgattctccg tttcgttatt ttagttgcgg taatgttgca     1080
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:58; N Pos. 9,12,18,24,27

Seq#:59; N Pos. 7,10,16,22,25

Seq#:67; Xaa Pos. 4,6,8,9,10,11,14,15,16,18,19,20,21,22,23,24,25,28,29,30

Seq#:67; Xaa Pos. 31,32,34,35,36,37,38,39,40,42,44,46,47,48,49,50,51,52,53

Seq#:67; Xaa Pos. 54,55,56,57,58,59,60,61,65,68,69,71,75

Seq#:68; Xaa Pos. 1,3,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,29

Seq#:68; Xaa Pos. 32,35,36,37,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53

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Seq#:68; Xaa Pos. 73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91

Seq#:68; Xaa Pos. 92,93,96

VERIFICATION SUMMARY

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L:4547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:4589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:5528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0
M:341 Repeated in SeqNo=67
L:5626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
M:341 Repeated in SeqNo=68